Remarks/Arguments

Claims 1-4 and 10-14 are pending in the application. Claims 1-4 and 10-14 have been rejected. Applicants respectfully request that the indicated amendments in the accompanying claims and new claims 17 and 18 be entered be entered for consideration

Claim Rejections – 35 USC §102

Claim 1 has been rejected under 35 U.S.C. 102(e) as being anticipated by Gu *et al.* (U.S. Patent No. 7,094,539). Claim 1 has been canceled in the newly-submitted listing of the claims that forms a part of this response.

Claim Rejections – 35 USC §112

Claims 1-4 and 10-14 have again been rejected under 35 U.S.C. 112, second paragraph, as indefinite. Claim 1 has been canceled. Claims 2-4 and 10-14 are not dependent upon claim 1. Rather, claims 2 and 10 are independent claims, with claims 3-4 and 11-14 being dependent upon claims 2 and 10, respectively. Applicants respectfully traverse the rejection of claims 2-4 and 11-14 because claims 2 and 10 do not contain the "group II intron-type reverse transcriptase" limitation which forms the basis of the examiner's rejection of these claims.

Claims 1-4 and 10-14 have been rejected under 35 U.S.C. 112, first paragraph, as containing subject matter supported by the discussion in the original disclosure. Claims 1 and 3 have been canceled in the newly-submitted claim listing. Claims 2 and 10 have been amended to recite "a variant of SEQ ID NO: 2 having at least 90% identity to SEQ ID NO: 2." Newly-submitted claim 17 recites "[a] substantially purified polypeptide as in claim 1, wherein the variant of SEQ ID NO: 2 has at least 95% identity to SEQ ID NO: 2." Newly-submitted claim 18 recites "[a] substantially purified polypeptide as in claim 1, wherein the variant of SEQ ID NO: 2 has at least 97% identity

to SEQ ID NO: 2." Support for these claim limitations may be found in the specification and in claims 2 and 10, as filed, which recited a variant with at least 80% identity to SEQ ID NO: 2, the range of variants with at least 80% identity inherently including those with at least 90%, 95%, and 97%. According to MPEP §2163.05, a claim limitation must be "expressly, implicitly, or inherently" supported in the specification. Citing *In re Wertheim*, 541 F.2d 257, 191 USPQ 90 (CCPA 1976), MPEP §2163.05 provides the example that where the ranges described in the original specification included a range of "25%- 60%" and specific examples of "36%" and "50%," a corresponding new claim limitation to "at least 35%" did not meet the description requirement because the phrase "at least" had no upper limit and caused the claim to read literally on embodiments outside the "25% to 60%" range, but a limitation to "between 35% and 60%" did meet the description requirement. In the present case, the term "at least 80%" encompasses from 80% to 100% sequence identity, with 90%-100% (*i.e.*, at least 90%), 95%-100% (*i.e.*, at least 95%), and 97% (*i.e.*, at least 97%) being within that range.

The level of skill of individuals who design and synthesize proteins is high. They are aware of the similarities and differences between the properties of certain amino acids. As shown in Figure 1 of the drawings which form a part of the application, the regions which appear to be required to be conserved are identified by the sequence comparison. There is a sufficient degree of variability between the non-conserved regions to allow one of skill in the art, given the disclosure provided by the present application, to modify a percentage of the amino acids in the polypeptide to provide an enzyme which retains the required conserved regions and the enzymatic activity associated with the Tirt polypeptide. Sequence comparison indicates that variation is tolerated in a number of the amino acid positions, while still producing a functional protein. Out of 420 amino acids in the polypeptide sequence of the protein, 90% sequence identity would require that 378 amino acids be identical between a polypeptide of SEQ ID NO: 2 and a variant; 95% sequence identity would require that 399 be identical; and 97% would require

that 407 be identical. The disclosure of the present application therefore enables one of skill in the art to provide a polypeptide having the required sequence identity, the disclosure identifying those amino acids which should be conserved in order to retain the protein's functionality.

The examiner stated that the specification is enabling for a reverse transcriptase comprising the amino acid sequence of SEQ ID NO: 2. For the above-mentioned reasons, Applicants submit that the specification is also enabling for a variant of the polypeptide having at least 90%, at least 95%, and/or at least 97% sequence identity SEQ ID NO: 2.

Respectfully submitted,

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I hereby certify that this correspondence is being deposited with the United States Postal Service, with sufficient postage as first class mail and addressed to Commissioner for Patents, United States Patent and Trademark Office, P.O. Box 1450, Alexandria, VA, on July 8, 2009.

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